Abstract

Methods for characterizing mutations in a polynucleotide are provided. Such methods comprise of separately ligating fragments of a reference polynucleotide and a target polynucleotide to identical or substantially identical arrays of polynucleotide probes having single-stranded overhangs constituting complete or substantially complete n-mer sets and comparing their hybridization patterns. The methods can also be used to detect the presence of polymorphisms. Methods are also provided to determine whether two or more polynucleotides of unknown sequences are identical. Further, methods are provided to enumerate and distinguish fragments of polynucleotides based on their terminal sequences. These methods are useful in medicine, pharmacogenomics, biochemistry, and forensic sciences.